

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2003, 19:05:45 ; Search time 229 Seconds
(without alignments)
5752.514 Million cell updates/sec

Title: US-09-692-257A-1

Perfect score: 488

Sequence: 1 cctaaaaatagtttcgtata.....gaagatggcgctggcgcata 488

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

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- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
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- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44.6	9.1	273	24 ABL71419	Corn tassell-derive
C 2	41	8.4	674	21 AAG61490	674 bp region of p
C 3	41	8.4	2796	6 AAN50036	Partial sequence o
C 4	41	8.4	4897	11 AAQ03259	Pseudorabies virus
C 5	40	8.2	11396	22 ABA17777	Human nervous syst
C 6	39.4	8.1	2742	19 AAV49291	Aujeszky's disease
C 7	38	7.8	465	24 ABL93562	Arabidopsis thalia
C 8	36.2	7.4	2064	14 AAQ52638	Streptomyces fradi

ALIGNMENTS

RESULT 1

ABL71419/C

ID ABL71419 standard; cDNA; 273 BP.

XX AC ABL71419;

XX AC ABL71419;

DT 14-MAY-2002 (first entry)

DE Corn tassell-derived polynucleotide (cdps) SEQ ID NO:793.

XX Corn; corn tassell-derived polynucleotide; cdps; hybrid breeding; CDPs;
inheriance; characteristic; growth; development; disease resistance;
environmental adaptability; quality; yield; molecular marker;
multigene trait; plant breeding; corn tassell; gene; ss.

OS Zea mays.

PN US2001051335-A1.

XX 13-DEC-2001.

PD 16-APR-1999; 99US-0294093.

XX 21-APR-1998; 98US-082567P.

PA (LALG/) LALGUDI R V.

PA (ITOL/) ITO L Y.

XX (SHER/) SHERMAN B K.

PI Lalgudi RV, Ito LY, Sherman BK;

Immunoglobulin C-g
Human cDNA encodin
S. spinosa DNA fra
S. spinosa DNA fra
DNA encoding Therm
NADP-specific glut
cDNA encoding matu
cDNA encoding matu
Glutamate dehydrog
NADP-glutamate deh
NADP-specific glut
NADP-glutamate deh
NADP-specific glut
cDNA encoding NADP
NADP-specific glut
NADP-specific glut
cDNA encoding NADP
Thermus caldophilu
Thermus caldophilu
B-domain-deleted-F
Human polynucleoti
Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
Barley dihydroquer
Eucalyptus grandis
Human gene trapped
DNA encoding novel
DNA encoding human
Human vesicle asso
Human cDNA sequenc
Human ORFX ORF1813
S. coelicolor fessW
Humanised F-RSV/HN
Humanised F-RSV/HN
Mouse laminin-15 g


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PF 17-JAN-2001; 2001WO-US01334.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
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PR 14-JUL-2000; 2000US-0218290.
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PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
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PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
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PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
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PR 06-SEP-2000; 2000US-0230437.
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PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
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PR 14-SEP-2000; 2000US-0233065.
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PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246476.
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PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
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PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
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PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
XX
```


PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYU/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHAW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICK/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX
 PI Goralach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX
 DR WPI: 2002-267486/31.
 XX
 XX
 PT New Arabidopsis thaliana nucleic acid, for identifying homologous
 PT genes, producing compositions that modulate the expression or function
 PT of its encoded protein, and mapping functional regions of a protein -
 XX
 PS Claim 1: SEQ ID 327: 44pp: English.
 XX
 CC The present invention describes an Arabidopsis thaliana nucleic acid (I)
 CC comprising a sequence capable of hybridising under stringent conditions
 CC to a sequence (S1) selected from any one of the 999 sequences given in
 CC ABU3336 to ABU94234. (I) have insecticide and fungicide activities, and
 CC they can be used as protein expression modulators. (I) can be used in
 CC identifying homologous or related genes, in producing compositions that
 CC modulate the expression or function of their encoded proteins, mapping
 CC functional regions of the proteins, and in studying associated
 CC physiological pathways. (I) can also be used: (1) for the genetic
 CC manipulation of cells, particularly plant cells; (2) in screening assays
 CC of various plant strains to determine the strains that are best capable
 CC of withstanding a particular disease or environmental stress; (3) for
 CC enhancing or inhibiting production of a biosynthetic product in a plant;
 CC (4) as probes in mapping and in diagnosis, in genetic modification and
 CC for screening purposes, to generate additional copies of the nucleic
 CC acids, to generate ribozymes or antisense oligonucleotides, and as
 CC single-stranded DNA probes or as triple-stand forming oligonucleotides;
 CC and (5) for generating genetically modified transgenic organisms.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site.
 XX
 SQ Sequence 465 BP; 149 A; 101 C; 97 G; 118 T; 0 other;
 Query Match 7.8%; Score 38; DB 24; Length 465;
 Best Local Similarity 52.5%; Pred. No. 0.22; Indels 0; Gaps 0;
 Matches 83; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
 QY 306 GGCAGGTGTTGTGGGACTGGCAGTGGCAGTGTGTGGCCGCGCAGCGAGAACCT 365
 DB III IIIIII III IIIIII III IIIIII III IIIIII III IIIIII
 273 GCGCAGTGTGTATGATTTTGCAGTTTGGGCACTTCTGAGCCACCATGCTGTACCT 332
 QY 366 GCGTCGTGTCCTCGCAGTGGTTCACACAGNCCCATCCCTTCCGCTGTACAGTGTG 425
 DB III IIIIII III IIIIII III IIIIII III IIIIII III IIIIII
 333 CTGCTTCTTCTCCACAGTGGTTCGACAGATCTGAACCATCTGTGTTCTGTGTTCTG 392
 QY 426 CTTCCATCTCTGCGTGGAGGCCCTTGAAGAACTGTGCC 463
 DB III III III IIIIII III IIIIII III IIIIII III IIIIII
 393 GCATTGGTGTAGCGGCAATCTCCATGTCAAACTTCTCC 430

RESULT 8

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 ID AAQ52638 standard; DNA; 2064 BP.
 XX
 AC AAQ52638;
 XX
 DT 25-MAR-2003 (updated)
 DT 02-JUN-1994 (first entry)
 XX
 DE Streptomyces fradiae glutamic acid-specific protease gene.
 XX
 KW endopeptidase; glutamic acid-specific protease; Sfase;
 KW protein sequencing; ds.
 XX
 OS Streptomyces fradiae (ATCC 14544).
 XX
 FH Key Location/Qualifiers
 FT -35_signal 359..364 /*tag= a
 FT -10_signal 378..383 /*tag= b
 FT CDS 435..1508 /*tag= c
 FT /*product= glutamic_acid-specific_endopeptidase
 FT sig_peptide 435..944 /*tag= d
 XX
 PN W09323530-AL.
 XX
 PD 25-NOV-1993.
 XX
 PF 30-APR-1993; 93WO-JP00592.
 XX
 PR 19-MAY-1992; 92JP-0126511.
 XX
 PA (SHIO) SHIONOGI SEIYAKU KK.
 XX
 PI Kitadokoro K, Nakamura E, Shin M, Teraoka H, Tsuzuki H;
 XX WPI: 1993-396564/48.
 DR P-PSDB; AAR44216.
 XX
 PT Protease which cleaves peptide(s) at glutamic acid residue
 PT C-terminal - is isolated from Streptomyces fradiae ATCC-14544
 XX
 PS Claim 5; Page 29-32; 41pp; Japanese.
 XX
 CC This sequence encodes a protease which cleaves on the C-terminal
 CC side of glutamic acid residues and was isolated from S. fradiae ATCC
 CC 14544 genomic DNA. The protease has an optimum pH of 8.2 and a stable
 CC pH range at 37 deg C of 6-9. It can be used for the analytical
 CC investigation of proteins or to cleave peptide chains at a defined
 CC site.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 2064 BP; 270 A; 859 C; 699 G; 236 T; 0 other;
 Query Match 7.4%; Score 36.2; DB 14; Length 2064;
 Best Local Similarity 48.3%; Pred. No. 1.5;
 Matches 101; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
 QY 276 GTGGCTACGAAGACGGGGGTGCCACCGGCAGGTGTGGGACTGGCAGTGGCAGC 335
 DB IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
 774 GTGCTCCAGGGGGCCATGGCGCTCGAGCTCGGGCGCGCGCTGACCCCGCGG 715
 QY 336 ACTTGTGGCCGCGCAGCGGAGAACCTGGTTCGTCCTCGTGTGAGTGTGACACGA 395
 DB IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
 714 GCGTGGCGCGCGCGCGGACCTTGGCGGCGCGGCGCTCGGTGTGAGTGTGACACGA 655
 QY 396 CCCATCCCTTCCCGTGTACAGTAGCTTGCCTCCATCTCTGGTCGAGGCGCTTGAAGA 455
 DB IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
 654 GTTCGCGCGTGGCGGCTCCAGTAGTGGCGGCTGTCTGTCGCGGAGGTCGCGTCGA 595
 QY 456 ACTTGTCCATGTGCAAGATGGCGTGGCG 484

XX SQ Sequence 1906 BP; 338 A; 671 C; 578 G; 319 T; 0 other;
 Query Match 7.4%; Score 36; DB 22; Length 1906;
 Best Local Similarity 62.0%; Pred. No. 1.6;
 Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 307 CGAGGTGTTGCGACTGGCAGTGGCAGCACTTGTGGCCGCGCACGCCGAGAGACCTG 366
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 Db 935 GCGGTGGTGTGTTGCTGGCAGCGGAGGCACTGGCCCGCCACCTGCGGGCCGCACTC 876
 || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

QY 367 CGTGTGTCCTCGAGTGTGTCACGACCC 398
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 Db 875 GCTGGCATGCCCTGTCACCTGCACCTGCGCGC 844

RESULT 11
 AAF88314/C
 ID AAF88314 standard; DNA: 25360 BP.
 XX AC AAF88314;
 XX DT 28-AUG-2001 (first entry)
 XX DE S. spinosa DNA fragment SEQ ID 3.
 XX KW Forosamine; trimethylrhannose; polyketide synthase; biosynthesis;
 KW spinosyn; polyketide aglycone; transgenic plant; insect resistance;
 KW macrolide; insecticidal; ds.
 XX OS Saccharopolyspora spinosa.
 XX PN DE19957268-A1.
 XX PD 08-MAR-2001.
 XX PF 29-NOV-1999; 99DE-1057268.
 XX PR 27-AUG-1999; 99DE-1040596.
 XX PA (FARB) BAYER AG.
 XX PI Eberz G, Moehrle V, Froede R, Velten R, Salas JA;
 XX DR WPI; 2001-267102/28.
 XX PT New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for
 PT recombinant production of insecticidal spinosyns and their derivatives
 PS Claim 7; Page 49-58; 354pp; German.
 XX CC This invention describes a novel method nucleic acid (I) and its encoded
 CC polypeptide (II) containing at least one region that encodes an enzymatic
 CC activity involved in biosynthesis of spinosyns. (I) are used (i) to
 CC identify, inactivate or modulate genes involved in the biosynthesis of
 CC (II); (ii) to generate a library of polyketide synthases; (iii) for
 CC adding forosamine or trimethylrhannose to a spinosyn or polyketide
 CC aglycone; and (iv) for recombinant production of the corresponding
 CC enzymes, which are used for production of (II), their precursors or
 CC derivatives, including production of transgenic plants that express (II)
 CC and thus have increased resistance to insects. (I) are also useful as
 CC markers for sequencing of the Saccharopolyspora spinosa genome. (II) are
 CC macrolides with insecticidal, but not antibacterial, activity, and can
 CC also be used to raise specific antibodies, useful for identifying
 CC expression clones in a gene bank. Cells transformed with (I) may produce
 CC (II) at significantly increased levels or produce new derivatives of
 CC genome which contains the coding regions for proteins involved in
 CC forosamine, trimethylrhannose and polyketide synthase biosynthesis.
 XX SQ Sequence 25360 BP; 3832 A; 9143 C; 8354 G; 4031 T; 0 other;

Query Match 7.4%; Score 36; DB 22; Length 25360;
 Best Local Similarity 48.1%; Pred. No. 4.9;
 Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 275 GGTGGTACGGAAGACGCGGGGTGCCACCCGCGAGGTGTGTGGACTGGCAGTGGCAG 334
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 Db 12735 GGTGTGCACAGATAGACGATCGGCTCCAGGTAGAGTTCACGAGTGCAGGAACGTGAAG 12676
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QY 335 CACTTGTGGCCCGCCGCGGAGAGACCTGGTGGTCTCCCTGCTGCTGTCACACG 394
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 12675 ATCGCACGCGCCGCGGCGGCGGAGACGCGGAGGCGCCACCGGTAGAGATGCCCC 12616
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QY 395 ACCCATCCCTTTCCTGTACAGTAGTTCCTCATCTCTCGCTCGAGGGCTTTGAAG 454
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 Db 12615 GCTCGTCCGAGGCCCTCCATCCGCGGCGCTCTCCAGTCCGACGCGAGGCGCATGAAG 12556
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QY 455 AACTTGTCCATGTGGAAGATGGCGTGGCGCA 486
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 Db 12555 AACTGGCGCATGATGAAGATCGCCACGACACA 12524

RESULT 12
 AAF88317/C
 ID AAF88317 standard; DNA: 29736 BP.
 XX AC AAF88317;
 XX DT 28-AUG-2001 (first entry)
 XX DE S. spinosa DNA fragment SEQ ID 6.
 XX KW Forosamine; trimethylrhannose; polyketide synthase; biosynthesis;
 KW spinosyn; polyketide aglycone; transgenic plant; insect resistance;
 KW macrolide; insecticidal; ds.
 XX OS Saccharopolyspora spinosa.
 XX PN DE19957268-A1.
 XX PD 08-MAR-2001.
 XX PF 29-NOV-1999; 99DE-1057268.
 XX PR 27-AUG-1999; 99DE-1040596.
 XX PA (FARB) BAYER AG.
 XX PI Eberz G, Moehrle V, Froede R, Velten R, Salas JA;
 XX DR WPI; 2001-267102/28.
 XX PT New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for
 PT recombinant production of insecticidal spinosyns and their derivatives
 PS Claim 7; Page 92-102; 354pp; German.
 XX CC This invention describes a novel method nucleic acid (I) and its encoded
 CC polypeptide (II) containing at least one region that encodes an enzymatic
 CC activity involved in biosynthesis of spinosyns. (I) are used (i) to
 CC identify, inactivate or modulate genes involved in the biosynthesis of
 CC (II); (ii) to generate a library of polyketide synthases; (iii) for
 CC adding forosamine or trimethylrhannose to a spinosyn or polyketide
 CC aglycone; and (iv) for recombinant production of the corresponding
 CC enzymes, which are used for production of (II), their precursors or
 CC derivatives, including production of transgenic plants that express (II)
 CC and thus have increased resistance to insects. (I) are also useful as
 CC markers for sequencing of the Saccharopolyspora spinosa genome. (II) are
 CC macrolides with insecticidal, but not antibacterial, activity, and can
 CC also be used to raise specific antibodies, useful for identifying
 CC expression clones in a gene bank. Cells transformed with (I) may produce
 CC (II) at significantly increased levels or produce new derivatives of
 CC genome which contains the coding regions for proteins involved in
 CC forosamine, trimethylrhannose and polyketide synthase biosynthesis.
 XX SQ Sequence 25360 BP; 3832 A; 9143 C; 8354 G; 4031 T; 0 other;

CC cDNA clones (AA764547 and AA764548) respectively code for the alpha
 CC (AAW15411) and beta mature subunits (AAW15412) of ammonium-inducible,
 CC chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-
 CC GDH) hexameric isoenzymes of *Chlorella sorokiniana*. They were
 CC obtd. by removal of the chloroplast targeting signal from full-
 CC length cDNA clones (see also AA764542-43) by PCR mutagenesis. The N
 CC metabolism of plant cells can be modulated (pref. increasing the
 CC assimilation of inorganic N into organic N) by transforming them
 CC with nucleotide sequences encoding the alpha and/or beta mature
 CC subunits or subunit precursors (see also AA764529-30). Such plants
 CC show improved properties, e.g. increased crop yield and improved
 CC stress tolerance. Heterohexamers having alpha and beta subunits
 CC can be expressed that have higher aminating/deaminating activity
 CC ratios (i.e. higher capacity for glutamate synthesis) than
 CC homohexamers.

XX
 SQ Sequence 1473 BP; 297 A; 486 C; 470 G; 220 T; 0 other;
 Query Match 7.3%; Score 35.6; DB 18; Length 1473;
 Best Local Similarity 49.5%; Pred. No. 2;
 Matches 92; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 287 AGACGGGGGGTCCACCCCGCAGGTGTTGGACTGGCAGTGGCAGCATTGTGGCC 346
 DB 1238 AGCCCGCTGACCCCGCAGCGCCGCGCTTGGCCGCTTGGCGGCGAGTAGATGCCG 1179
 QY 347 GCCACGCCGAGAGACCTGCGTGTCTCCCTGCAGTCGTCACACGACCCATCCCTTT 406
 DB 1178 GCCTTGTGTACTGTGGATGGCTGCTGGTGAGGGCAATGTGGCGCCCTCCACGACG 1119
 QY 407 CCCGTGTACAAAGTAGCTTGCTCCATCTCTGCTCGAGGGCCCTTGAAGAACTTGTCCATG 466
 DB 1118 TACTGGCAGCGGTGCTTGATCAGCAGCTCGGCGCTGCTCATCGATCTCGTTCTGGTG 1059
 QY 467 TCGAAG 472
 DB 1058 GCGCAG 1053

RESULT 15
 ABK51026/C
 ID ABK51026 standard; cDNA; 1473 BP.
 XX AC ABK51026;
 XX
 XX 24-SEP-2002 (first entry)
 XX cDNA encoding mature NADP-glutamate dehydrogenase beta subunit.
 XX NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit;
 KW alga; nitrogen metabolism; plant; ammonium assimilation; transgenic;
 KW ammonia toxicity tolerance; osmotic stress tolerance; gene; ss.
 XX *Chlorella sorokiniana*.
 XX
 XX Key Location/Qualifiers
 FT CDS 4..1434
 FT /*tag= a
 FT /product= "Mature NADP-specific glutamate dehydrogenase
 FT beta subunit"
 XX
 XX US2002062495-A1.
 XX
 XX 23-MAY-2002.
 XX
 XX 01-MAY-1998; 98US-0070844.
 XX
 XX 01-MAY-1998; 98US-0070844.
 XX
 XX (SCHM/) SCHMIDT R R.
 PA (MILL/) MILLER P.
 XX
 XX Schmidt RR, Miller P;
 PI

XX WPI; 2002-499691/53.
 DR P-PSDB; AAU98955.
 XX
 PT Transforming a plant with a polynucleotide encoding a polypeptide with
 PT glutamate dehydrogenase activity provides a plant with modulated
 PT nitrogen metabolism useful to increase yield and ammonium and osmotic
 PT stress tolerance
 XX
 XX Example 2; Page 31-32; 35pp; English.
 XX
 XX The invention relates to a method of modulating nitrogen metabolism in
 CC plant cells, comprising transforming a plant cell with a polynucleotide
 CC encoding a polypeptide having glutamate dehydrogenase activity, and
 CC culturing the cell to produce descendant cells which express the
 CC polypeptide. The method is used to provide plants with increased yield,
 CC improved ammonium assimilation properties, increased tolerance to
 CC ammonia toxicity, improved osmotic stress tolerance and improved
 CC composition. The present sequence represents the coding sequence of
 CC mature *Chlorella sorokiniana* NADP-glutamate dehydrogenase beta subunit.
 CC used in the method of the invention.

XX
 SQ Sequence 1473 BP; 297 A; 486 C; 470 G; 220 T; 0 other;
 Query Match 7.3%; Score 35.6; DB 24; Length 1473;
 Best Local Similarity 49.5%; Pred. No. 2;
 Matches 92; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 287 AGACGGGGGGTCCACCCCGCAGGTGTTGGACTGGCAGTGGCAGCATTGTGGCC 346
 DB 1238 AGCCCGCTGACCCCGCAGCGCCGCGCTTGGCCGCTTGGCGGCGAGTAGATGCCG 1179
 QY 347 GCCACGCCGAGAGACCTGCGTGTCTCCCTGCAGTCGTCACACGACCCATCCCTTT 406
 DB 1178 GCCTTGTGTACTGTGGATGGCTGCTGGTGAGGGCAATGTGGCGCCCTCCACGACG 1119
 QY 407 CCCGTGTACAAAGTAGCTTGCTCCATCTCTGCTCGAGGGCCCTTGAAGAACTTGTCCATG 466
 DB 1118 TACTGGCAGCGGTGCTTGATCAGCAGCTCGGCGCTGCTCATCGATCTCGTTCTGGTG 1059
 QY 467 TCGAAG 472
 DB 1058 GCGCAG 1053

Search completed: September 12, 2003, 00:07:47
 Job time : 234 secs